A. The mass spectrometry analysis of phosphorylation sites in HBE cell

Phosphorylation sites	Peptide sequence
T170	RT#SDPRL
S171	RTS#DPRL
T185	KECMDMLRLT#LQTTSDGVMLDKD
S242	KKQS#GGKV
S380	KMAGNEYVGFSNATFQS#ERE
S593	RMES#LGERS

B. The mass spectrometry analysis of phosphorylation sites in H1299 cell

Phosphorylation sites	Peptide sequence
T112	KDSPGET#DAFGNSEGKEMVAAGDNKIKQ
S171	RTS#DPRL
T185	RLT#LQTTSDGVMLDKD
T188	RLTLQT#TSDGVMLDKD
S274	RHS#IGDTKV
T278	RHSIGDT#KV
S314	KEPS#GLRFNKL
S511	KMGNS#VKG
S576	KKVS#PESSDDTSTTVVYRMESLGERS
S593	RMES#LGERS

C. Comparing the phosphorylation sites in H1299 with HBE cells

HBE	H1299
T170	T112
S171	S171
T185	T185
S242	T188
S380	S274
S593	T278
	S314
	S511
	S576
	S593

Table S1. The GAC phosphorylation sites in HBE cells and H1299 cells. **(A)** The mass spectrometry analysis of GAC phosphorylation sites in HBE cells. **(B)** The mass spectrometry analysis of GAC phosphorylation sites in H1299 cells. **(C)** Comparing the GAC phosphorylation sites in H1299 cells with those in HBE cells from the mass spectrometry analysis results.